

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 24, 2003, 15:48:45 ; Search time 22.0606 Seconds

(without alignments)
1133.013 Million cell updates/sec

Title: US-09-988-971-2_COPY_2_261

Perfect score: 1346
Sequence: 1 GSLPSRRKSLPSPLSSVQ.....RESLSFYISLNDFAVSLDDA 260

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	497.5	37.0	281	2 A57152	src-like adaptor p
2	374.5	27.8	512	1 TVHULY	protein-tyrosine k
3	371.5	27.6	512	1 I56160	protein-tyrosine k
4	371.5	27.6	512	1 A39719	protein-tyrosine k
5	364.5	27.1	505	1 TVHJHC	protein-tyrosine k
6	356.5	26.5	505	2 I37206	protein-tyrosine k
7	356.5	26.4	503	1 TVMSHC	protein-tyrosine k
8	355.5	26.4	503	1 JQ1321	protein-tyrosine k
9	345.5	25.7	499	1 A40092	protein-tyrosine k
10	344.5	25.6	509	1 OKHOLK	protein-tyrosine k
11	342.5	25.4	509	1 I48845	protein-tyrosine k
12	337.5	25.0	507	1 A39939	protein-tyrosine k
13	329.5	24.4	539	2 B49114	protein-tyrosine k
14	324.5	24.1	528	1 TVFVG9	protein-tyrosine k
15	323.5	24.0	537	1 A45501	protein-tyrosine k
16	321.5	23.8	541	1 TVCHIS	protein-tyrosine k
17	319.5	23.7	537	1 TVHUSY	protein-tyrosine k
18	319.5	23.5	543	1 TVHUSY	protein-tyrosine k
19	316.5	23.5	529	1 TVHUSY	protein-tyrosine k
20	315.5	23.4	544	2 I51593	protein-tyrosine k
21	314.5	23.4	537	1 A43806	protein-tyrosine k
22	313.5	23.3	534	1 A44991	protein-tyrosine k
23	311.5	23.1	517	2 S24547	protein-tyrosine k
24	309.5	23.0	537	2 I51592	protein-tyrosine k
25	309.5	23.0	541	2 S31845	protein-tyrosine k
26	305.5	22.7	517	2 A43807	protein-tyrosine k
27	305.5	22.7	536	2 S33569	protein-tyrosine k
28	301.5	22.4	534	1 S33568	protein-tyrosine k
29	299.5	22.3	542	2 A49114	protein-tyrosine k

30	294	21.8	506	1 S24553	protein-tyrosine k
31	290.5	21.6	557	1 TVFVS2	protein-tyrosine k
32	290.5	21.6	587	1 TVFVPR	protein-tyrosine k
33	288.5	21.4	533	1 TVCHIS	protein-tyrosine k
34	288.5	21.4	568	1 TVFVS1	protein-tyrosine k
35	283.5	21.1	526	1 TVFV60	protein-tyrosine k
36	280	20.8	509	1 TVHAST	protein-tyrosine k
37	279	20.7	546	2 S52314	protein-tyrosine k
38	278.5	20.7	532	1 B34104	protein-tyrosine k
39	277.5	20.6	526	1 TVFVR	protein-tyrosine k
40	277.5	20.6	526	2 S15582	protein-tyrosine k
41	277.5	20.6	542	1 TVHUSC	protein-tyrosine k
42	277.5	20.6	545	2 S52313	protein-tyrosine k
43	275.5	20.5	532	1 A34104	protein-tyrosine k
44	275.5	20.5	541	1 A34104	protein-tyrosine k
45	273.5	20.3	526	2 S24520	protein-tyrosine k

ALIGNMENTS

RESULT 1

A57152
src-like adaptor protein - mouse
C/Species: Mus musculus (house mouse)
C/Date: 08-Dec-1995 #sequence_rev1510 08-Dec-1995 #text_change 12-Feb-1999
C/Accession: A57152
J. Pandey, A.; Duan, H.; Dixit, V. M.
J. Biol. Chem. 270, 19201-19204, 1995
A/Title: Characterization of a novel Src-like adaptor protein that associates with the F-29-77/Domain: SH3 homology <SH3>
A/Reference number: A57152, MUID:95370243; PMID:7543898
A/Accession: A57152
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-281 <PAN>
A/Cross-references: GB:U29056
A/Suprafamily: SH3 homology; SH2 homology
F:29-77/Domain: SH3 homology <SH3>
F:84-175/Domain: SH2 homology <SH2>

Query Match 37.0%; Score 497.5; DB 2; Length 281;
Best Local Similarity 43.9%; Pred. No. 1.3e-33;
Matches 116; Conservative 38; Mismatches 81; Indels 29; Gaps 7;

QY 8 KSLPS--LSSVQGPVTWEAERSKATVALGSPGAPGAEUSLRLEPTLTVS2D 64
DB 6 KSLPSRRKSLSS-----EGLESDPLAV-LTVPSDDISPIFRGKRLVSD 55
QY 65 GDMWTVLSVSGREYNIPSVYAKVSHGMYBGLSREKAEELLPLGNGCAFIRE2QT 124
DB 56 GGMWKAISLSTRESYIPGCVARVYHGLFEGIGRKAEBELLQPDRTIGSFMIRES2T 115
QY 125 RRGYSLSVRLRPASMDRIHRYHICDNGLYISRLTFP2LOALVDHYSELDIDC 184
DB 116 KKGYSLSVR-----HRQYKHRIIRLPMNMYIISRLTFQCELDVYTHSEVADLCC 169
QY 185 LKAPCVLR-----AGPLPKDIPVPTVQRTPLANKELDLSLFSEATG---EST 235
DB 170 VLTPTCLANTIPAPTSHPSPCTSPGSPVTLRQKTFDMKRVSRLOBSGEGANPLRVDES 229
QY 236 LSEGLRESLSFYISL-NDFAVSLD 258
DB 230 FSYGLRESLSFYISLITGDDSSFD 253

RESULT 2

TVHULY
protein-tyrosine kinase (EC 2.7.1.112) 1yn, splice form A - human
N/Contains: protein-tyrosine kinase 1yn, splice form B
C/Species: Homo sapiens (man)
C/Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 18-Feb-2000
C/Accession: A26719; D38268; P09499; I53715
R.Yamanashi, Y.; Fukushige, S.I.; Semba, K.; Sukegawa, J.; Miyajima, N.; Matsubara, K.;

Mol. Cell. Biol. 7, 237-243, 1987

A:Title: The yes-related cellular gene lyn encodes a possible tyrosine kinase similar to

A:Reference number: A26719; MUID:87172710; PMID:1561390

A:Accession: A26719

A:Molecule type: mRNA

A:Residues: 1-512 <YAM>

A:Cross-references: GB:M16038; NID:G187268; PIDN:AAA59540.1; PID:G307144

A:Partanen, J.; Mäkelä, T.P.; Allitalo, R.; Lehtela, H.; Allitalo, K.

Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990

A:Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.

A:Reference number: A38268; MUID:91062389; PMID:2247464

A:Accession: D38268

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 369-424 <PAR>

A:Biochem. Biophys. Res. Commun. 186, 1403-1409, 1992

A:Title: Expression of the B cell-associated tyrosine kinase gene lyn in primary neurobl

A:Reference number: PH0949; MUID:92378604; PMID:1510669

A:Accession: PH0949

A:Molecule type: mRNA

A:Residues: 369-424 <BIB>

A:Experimental source: neuroblastoma SK-IN cell

A:Rider, L.G.; Raben, N.; Miller, L.; Jelsema, C.

Gene 138, 219-222, 1994

A:Title: The cdnas encoding two forms of the lyn protein tyrosine kinase are expressed

A:Reference number: 153715; MUID:94171041; PMID:8125304

A:Accession: 153715

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-24, 46-512 <RID>

A:Cross-references: GB:M79321; NID:G187270; PIDN:AAA50019.1; PID:G187271

A:Experimental source: splice form B

A:Gene: GDB:LYN

A:Cross-references: GDB:120159; OMIM:165120

A:Map position: 8q13-qter

C:Function: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP

A:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h

C:Keywords: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprote

tyrosine-specific protein kinase

F:2-512/Product: protein-tyrosine kinase lyn, splice form A #status predicted <MATA>

F:2-24, 46-512/Product: protein-tyrosine kinase lyn, splice form B #status predicted <MATA>

F:70-118/Domain: SH2 homology <SH3>

F:129-226/Domain: SH2 homology <SH2>

F:245-504/Domain: protein kinase homology <KIN>

F:253-261/Region: protein kinase ATP-binding motif

F:12/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F:13/Binding site: palmitate (Cys) (covalent) #status predicted

F:275/Active site: lys #status predicted

F:397,508/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 27.8%; Score 374.5; DB 1; Length 512;

Best Local Similarity 40.3%; Pred. No. 3; Be-23;

Matches 81; Conservative 36; Mismatches 75; Indels 9; Gaps 3;

5 SRRKSLPSPSSSVQGGPYTMEARSKATVALGSPAGGPAELSLRLGEPPLTVSD 64

38 SNKQRPVPE-SQLPGORFPOKDPBOGDIVVALPYDGHDPDLSFKKGKVKVLEEH 96

65 GDMWTVLSEVSGREYNIPSVYAKV---SHGWLVEGLSREKAEELLLPGNPGAFILR 120

97 GEMWAKSLTKKEGFTSNVAKVLTLEEMFFDITRKDAERQLLAQNSAGAFILR 156

121 ESQTRGYSYLSVRLSPASWDRIIRYHICLDNGWLYISPLTSPSLQALVDYSELAD 180

157 ESETLKGSFSLSVRFDVHGDVYIKYKIRSLDNGYISPRITPCISDMIKYKQAD 216

181 DICCLKEPCVLORAGPLPGK 201

217 GLCRLEKACI-----SPKPK 233

RESULT 3

156160 protein-tyrosine kinase (EC 2.7.1.112) lyn, splice form A - rat

N:Contains: protein-tyrosine kinase lyn, splice form B

C:Species: Rattus norvegicus (Norway rat)

C:Date: 18-Feb-2000 #sequence revision 18-Feb-2000 #text_change 18-Feb-2000

C:Accession: 156160; 167811; 167812

R:Minoguchi, K.; Nishikata, H.; Stragmanian, R.P.

J. Immunol. 150, 222, 1993

A:Title: Bacterially expressed rat p56lyn binds several proteins in rat basophilic leuk

A:Reference number: 156160

A:Accession: 156160

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-512 <MIN>

A:Cross-references: GB:L1951; NID:G294582; PIDN:AAA41549.1; PID:G294583

A:Rider, L.G.; Raben, N.; Miller, L.; Jelsema, C.

Gene 138, 219-222, 1994

A:Title: The cdnas encoding two forms of the lyn protein tyrosine kinase are expressed

A:Reference number: 153715; MUID:94171041; PMID:8125304

A:Accession: 167811

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-230, 'L', 232-307, 'A', 309-418, 'Y', 420-512 <RID>

A:Cross-references: GB:L14823; NID:G294580; PIDN:AAA20945.1; PID:G294581

A>Note: in Genbank entry RATTYNMYR, release 116.0, PIDN:AAA20945.1, the source is desig

C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h

C:Keywords: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprote

F:2-512/Product: protein-tyrosine kinase lyn, splice form A #status predicted <MATA>

F:2-24, 46-512/Product: protein-tyrosine kinase lyn, splice form B #status predicted <MATA>

F:70-118/Domain: SH3 homology <SH3>

F:129-226/Domain: SH2 homology <SH2>

F:245-504/Domain: protein kinase homology <KIN>

F:253-261/Region: protein kinase ATP-binding motif

F:12/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F:13/Binding site: lys #status predicted

F:397,508/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 27.6%; Score 371.5; DB 1; Length 512;

Best Local Similarity 40.8%; Pred. No. 6; Be-23;

Matches 82; Conservative 33; Mismatches 77; Indels 9; Gaps 3;

5 SRRKSLPSPSSSVQGGPYTMEARSKATVALGSPAGGPAELSLRLGEPPLTVSD 64

38 SNKQRPVPE-SQLPGORFPOKDPBOGDIVVALPYDGHDPDLSFKKGKVKVLEEH 96

65 GDMWTVLSEVSGREYNIPSVYAKV---SHGWLVEGLSREKAEELLLPGNPGAFILR 120

97 GEMWAKSLTKKEGFTSNVAKVLTLEEMFFDITRKDAERQLLAQNSAGAFILR 156

121 ESQTRGYSYLSVRLSPASWDRIIRYHICLDNGWLYISPLTSPSLQALVDYSELAD 180

157 ESETLKGSFSLSVRFDVHGDVYIKYKIRSLDNGYISPRITPCISDMIKYKQAD 216

181 DICCLKEPCVLORAGPLPGK 201

217 GLCRLEKACI-----SPKPK 233

RESULT 4

A39719 protein-tyrosine kinase (EC 2.7.1.112) lyn, long splice form - mouse

N:Contains: protein-tyrosine kinase lyn, short splice form

C:Species: Mus musculus (house mouse)

C:Date: 18-Feb-2000 #sequence revision 18-Feb-2000 #text_change 03-Mar-2000

C:Accession: A39719; B39719; A39750; B39750

R:Stanley, E.; Ralph, S.; McEwen, S.; Boulet, I.; Holzman, D.A.; Lock, P.; Dunn, A.R.
 Mol. Cell. Biol. 11, 3399-3406, 1991
 A>Title: Alternatively spliced murine lyn mRNAs encode distinct proteins.
 A:Reference number: A39719; MUID:91260688; PMID:1710766
 A:Accession: A39719
 A:Molecule type: mRNA
 A:Residues: 1-512 <STA2>
 A:Cross-references: GB:M64608; NID:g198938; P1DN:AAA3470.1; PID:g198939
 A:Accession: B39719
 A:Molecule type: mRNA
 A:Residues: 1-24, 46-512 <STA2>
 A:Cross-references: GB:M64608
 R:Yl, T.; Bolen, J.B.; Ihle, J.N.
 Mol. Cell. Biol. 11, 2391-2398, 1991
 A>Title: Hematopoietic cells express two forms of lyn kinase differing by 21 amino acids
 A:Reference number: A39750; MUID:91203857; PMID:2017160
 A:Accession: A39750
 A:Molecule type: mRNA
 A:Residues: 1-76, 'F', '78-160, 'I', '162-278, 'L', '280-390, 'I', '392-424, 'D', '426-512 <Y11>
 A:Cross-references: GB:M57696; NID:g198940; P1DN:AAA3471.1; PID:g198941
 A:Accession: B39750
 A:Molecule type: mRNA
 A:Residues: 1-24, 46-76, 'F', '78-160, 'I', '162-278, 'L', '280-390, 'I', '392-424, 'D', '426-512 <Y12>
 A:Cross-references: GB:M57697; NID:g198942; P1DN:AAA3472.1; PID:g198943
 C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h
 C:Keywords: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprote
 F.1-512/Product: protein-tyrosine kinase lyn, long splice form #status predicted <MATL>
 F.1-24, 46-512/Product: protein-tyrosine kinase lyn, short splice form #status predicted
 F.70-118/Domain: SH3 homology <SH3>
 F.123-226/Domain: SH2 homology <SH2>
 F.245-504/Domain: protein kinase homology <KIN>
 F.253-261/Region: protein kinase ATP-binding motif
 F.2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F.275/Active site: Lys #status predicted
 F.397,508/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 27.6%; Score 371.5; DB 1; Length 512;
 Best Local Similarity 40.8%; Pred. No. 6, 8e-23;
 Matches 82; Conservative 33; Mismatches 77; Indels 9; Gaps 3;

QY 5 SRRKSLPSPSSVQGGPVTMEARSKATVVALGSPGAPAEISLGLPEPLTIVSEED 64
 DB 38 SNKQRPVPEF-HLPQGRFQTKDPEQGDIVVLYALYDVAIHEDLSFKGQVAVLEESGEMWKA 96
 QY 65 GDMWTVLSEVSGREYNIPSVHAKV---SHGWLVEGLSREKAEELLPLPGNPGAPFLIR 120
 DB 97 GEMWKAQSSSKREGEIPSNVYAVKNTLETETEFKDTTRKDAERQLAPGNSAGAPFLIR 156
 QY 121 ESQTRGSSVLSVRLSPASMDRIHRYRHICLDNGMXYISPRITLFPISGLQALVDHSEAD 180
 DB 157 ESETLKGFSLSVRYDPMHGDVYKHKIRSLDNGGYITISPRITFPCISDMTKHYKQKSD 216
 QY 181 DICCLKEPCVLPQRAGPLPK 201
 DB 217 GLCRLEKACI----SPKPK 233

RESULT 5
 TVHHC
 protein-tyrosine kinase (EC 2.7.1.112) hck - human
 C:Species: Homo sapiens (man)
 C:Date: 31-Dec-1989 #sequence_revision 10-Nov-1995 #text_change 11-Jun-1999
 C:Accession: A27811; A27812; J01419; C38268; S31103
 R:Quintrell, N.; Lebo, R.; Varnum, H.; Bishop, J.M.; Pectinati, M.J.; Le Beau, M.M.; Dig
 Mol. Cell. Biol. 7, 2267-2275, 1987
 A>Title: Identification of a human gene (HCK) that encodes a protein-tyrosine kinase and
 A:Reference number: A27811; MUID:87257942; PMID:3496523
 A:Accession: A27811
 A:Molecule type: mRNA
 A:Residues: 1-505 <QUT>
 A:Cross-references: GB:M16591
 A>Note: the codon given for 3-Cys (TGC) is inconsistent with the authors' translation
 R:Ziegler, S.F.; Marth, J.D.; Lewis, D.B.; Perlmutter, R.M.

Mol. Cell. Biol. 7, 2276-2285, 1987
 A>Title: Novel protein-tyrosine kinase gene (hck) preferentially expressed in cells of
 A:Reference number: A27812; MUID:87257943; PMID:3453117
 A:Accession: A27812
 A:Molecule type: mRNA
 A:Residues: 1-505 <ZIR>
 A:Cross-references: GB:M16592; NID:g193913; P1DN:AAA2644.1; PID:g306833
 R:Hardy, D.; Schreiner, K.; Ruedemann-Waigmann, H.
 Gene 113, 275-280, 1992
 A>Title: The genomic locus of the human hemopoietic-specific cell protein tyrosine kinase
 A:Reference number: J01419; MUID:92241680; PMID:1572549
 A:Accession: J01419
 A:Molecule type: DNA
 A:Residues: 157-505 <HRA>
 A:Cross-references: EMBL:X5741
 R:Partanen, U.; Maekela, T.P.; Allitalo, R.; Leivaesalaho, H.; Allitalo, K.
 Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990
 A>Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.
 A:Reference number: A38268; MUID:91062389; PMID:2247464
 A:Accession: C38268
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 362-417 <PAR>
 C:Genetics: HCK
 A:Gene: GDB:HCK
 A:Cross-references: GDB:119303; OMIM:142370
 A:Map position: 20q11-20q12
 A:Insertions: 207/1; 258/1; 318/1; 343/3; 395/1; 439/1
 C:Function:
 A:Description: catalyzes the phosphorylation of a peptide tyrosine residue by ATP
 C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h
 C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phos
 F.2-505/Product: protein-tyrosine kinase hck #status predicted <MAT>
 F.64-112/Domain: SH3 homology <SH3>
 F.123-220/Domain: SH2 homology <SH2>
 F.239-497/Domain: protein kinase homology <KIN>
 F.247-255/Region: protein kinase ATP-binding motif
 F.2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F.3/Binding site: palmitate (Cys) (covalent) #status predicted
 F.269/Active site: Lys #status predicted
 F.390/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 27.1%; Score 364.5; DB 1; Length 505;
 Best Local Similarity 42.2%; Pred. No. 2, 5e-22;
 Matches 78; Conservative 31; Mismatches 69; Indels 7; Gaps 2;

QY 11 PPSLSVSSVQGGPVTMEARSKATVVALGSPGAPAEISLGLPEPLTIVSEEDGMWTV 70
 DB 40 PGRSNHS---NTFEIRAGSEDIIVVLYDVAIHEDLSFKGQVAVLEESGEMWKA 96
 QY 71 LSEVSGREYNIPSVHAKV---SHGWLVEGLSREKAEELLPLPGNPGAPFLIR 126
 DB 97 RSLATREKEGYIPSNVYAVKNTLETETEFKDTTRKDAERQLAPGNSAGAPFLIR 156
 QY 127 GSYSLSVRLSPASMDRIHRYRHICLDNGMXYISPRITLFPISGLQALVDHSEAD 186
 DB 157 GSYSLSVRYDPMHGDVYKHKIRSLDNGGYITISPRITFPCISDMTKHYKQKSD 216
 QY 187 KEPCV 191
 DB 217 SVPCM 221

RESULT 6
 I37206
 protein-tyrosine kinase (EC 2.7.1.112) blk - human
 C:Species: Homo sapiens (man)
 C:Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 04-Mar-2000
 C:Accession: I37206; S51647
 R:Islam, K.B.; Rabbani, H.; Larsson, C.; Sanders, R.; Smith, C.I.
 J. Immunol. 154, 1265-1272, 1995
 A>Title: Molecular cloning, characterization, and chromosomal localization of a human ly
 A:Reference number: I37206; MUID:95123078; PMID:7822795

A:Accession: J13206
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-505 <RES>
A:Cross-references: EMBL:233998; NID:9601951; PIDN:CAA83965.1; PID:9601952
C:Genetics:
A:Gene: GDB:BLK
A:Cross-references: GDB:454114; OMIM:191305
A:Map position: 8p23-8p22
C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h
C:Keywords: ATP; blocked amino end; lipoprotein; myristylation; phosphotransferase; tyrc
F:124-220/Domain: SH2 homology <SH2>
F:65-113/Domain: SH3 homology <SH3>
F:239-497/Domain: protein kinase homology <KIN>
F:247-255/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:269/Active site: Lys #status predicted

Query Match 26.5%; Score 356.5; DB 2; Length 505;
Best Local Similarity 44.2%; Pred. No. 1.2e-21;
Matches 76; Conservative 24; Mismatches 67; Indels 5; Gaps 2;
Qy 24 PYTMEARSKATAVAGSPAGPAELSLRGEPLTIVSEDDWMTVLSEVSGREYNITS 83
Db 51 PRDEHDEDKHFFVALYDYAMNDRDLQMLKGEKLOVLTGTDWMLARSLVTGEGVPS 110
Qy 84 VHYAKV---HGMVYEGSLREKAEELLPGNPGAPLIRSGTFRSGSYSLRSPRA 139
Db 111 NFVARVESLEMERFNSGCKAEKQALAPINAGSFLIRSEINKAFSLSK-DVTT 169
Qy 140 SMDRIHRYHICLDNGMLYISPLTFPSLQALVDHYSELADDI CCLKEPCV 191
Db 170 QGBLKHVYKIRCLDEGCVYISPRITFPSLQALVQHSKKGDGLCORLTLPV 221

RESULT 7

TWNSHC
protein-tyrosine kinase (EC 2.7.1.112) hck - mouse
N:Alternate names: kinase-related transforming protein (bmk)
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 28-Jan-2000
C:Accession: A27282; A39973
R:Klemaz, M.J.; McKercher, S.R.; Maki, R.A.
Nucleic Acids Res. 15, 9600, 1987
A:Title: Nucleotide sequence of the mouse hck gene.
A:Reference number: A27282; PMID:88067781; PMID:3684607
A:Accession: A27282
A:Molecule type: mRNA
A:Residues: 1-503 <RES>
A:Cross-references: GB:Y00487; NID:951209; PIDN:CAA68544.1; PID:951210
R:Hotzman, D.A.; Cook, W.D.; Dunn, A.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 8325-8329, 1987
A:Title: Isolation and sequence of a cDNA corresponding to a src-related gene expressed
A:Reference number: A39973; PMID:8806887; PMID:3317404
A:Accession: A39973
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-503 <HOL>
A:Cross-references: GB:J03023; NID:9192212; PIDN:AAA7305.1; PID:9309118
C:Genetics:
A:Gene: hck
C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h
C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phd
F:162-110/Domain: SH3 homology <SH3>
F:121-218/Domain: SH2 homology <SH2>
F:237-495/Domain: protein kinase homology <KIN>
F:245-253/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:267/Active site: Lys #status predicted
F:388/499/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match

26.4%; Score 356; DB 1; Length 503;

Best Local Similarity 41.5%; Pred. No. 1.3e-21;
Matches 83; Conservative 33; Mismatches 72; Indels 12; Gaps 4;
Qy 10 LPSPSSSVQOGCVTWE---AERSKAT-AVALGSPAGPAELSLRGEPLTIVSEDDG 65
Db 30 VPDTSSSKLGNNSNSMPPEFGESEDTIVVALDYDEAIHREDLSFOKGDQMVLEAG 89
Qy 66 DWMTVLSEVSGREYNITPSVHAKV---SHGMVYEGSLREKAEELLPGNPGAPLIRE 121
Db 90 EMMVARSALATKEGYIPSNVAVYNSLLETFEWFPGJSRQDAERHLAPGNMUGSFMRD 149
Qy 122 SGTGRGYSYSLVRLSRPASMDRIRHYHICLDNGMLYISPLTFPSLQALVDHYSELADD 161
Db 150 SETTKGSYSLRPRDDPQHGTIVKHVYKIRLDSGGFYISPRITFSSLQELVLYHKKMGD 209
Qy 182 ICCLKEPCVLRQAPLRGK 201
Db 210 LCOKLSVPCV---SPKPOK 225

RESULT 8

J01321
protein-tyrosine kinase (EC 2.7.1.112) hck - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C:Accession: J01321; S18974
R:Okano, Y.; Sugimoco, Y.; Fukuoaka, M.; Matsui, A.; Nagata, K.; Nozawa, Y.
Biochem. Biophys. Res. Commun. 181, 1137-1144, 1991
A:Title: Identification of rat cDNA encoding hck tyrosine kinase from megakaryocytes.
A:Reference number: J01321; PMID:92109719; PMID:1764064
A:Accession: J01321
A:Molecule type: mRNA
A:Residues: 1-503 <RES>
A:Cross-references: GB:S74141; NID:9241436; PIDN:AAB20754.1; PID:9241437
A:Experimental source: megakaryocyte
R:Rema, V.; Swarup, G.
Submitted to the EMBL Data Library, December 1991
A:Reference number: S18974
A:Accession: S18974
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-50, 'V', 52-204, 'R', 206-305, 'T', 307-503 <RES>
A:Cross-references: EMBL:X62345; NID:957581; PIDN:CAA44218.1; PID:957582
C:Genetics:
A:Gene: hck
C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h
C:Keywords: ATP; autophosphorylation; blocked amino end; kinase-related transforming pro
n kinase
F:62-110/Domain: SH3 homology <SH3>
F:121-218/Domain: SH2 homology <SH2>
F:237-495/Domain: protein kinase homology <KIN>
F:245-253/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:3/Binding site: palmitate (Cys) (covalent) #status predicted
F:267/Active site: Lys #status predicted
F:388/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match

26.4%; Score 355.5; DB 1; Length 503;

Best Local Similarity 41.4%; Pred. No. 1.4e-21;

Matches 84; Conservative 32; Mismatches 72; Indels 15; Gaps 4;

Qy 4 PSRRSLPSPLSSVQOGCVTWEARSKAT-AVALGSPAGPAELSLRGEPLTIVS 62
Db 33 PISPKKLDPNSINSLPFG-----FVEGSEDTIVVALDYDEAIHREDLSFOKGDQMVLE 86
Qy 63 EDGDWMTVLSEVSGREYNITPSVHAKV---SHGMVYEGSLREKAEELLPGNPGAPL 118
Db 87 ESEEMWAKRSALATKEGYIPSNVAVYNSLLETFEWFPGJSRQDAERHLAPGNMUGSFM 146
Qy 119 IRESQTRGYSYSLVRLSRPASMDRIRHYHICLDNGMLYISPLTFPSLQALVDHYSEL 178
Db 147 IRSETTKGSYSLVRFDPQHGTIVKHVYKIRLDSGGFYISPRITFSSLQELVLYHKKMG 206

Qy 179 ADDICLLKEPCVLRAGPLPGK 201
Db 207 KDGCLQKLSVPCV-----SRFQK 225

RESULT 9

A:Accession: A40092
protein-tyrosine kinase (EC 2.7.1.112) blk [validated] - mouse
C:Species: Mus musculus (house mouse)
C>Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 16-Jun-2000
C:Accession: A40092
R:Lybeck, S.M.; Niederhuber, J.E.; Desiderio, S.V.
Science 247, 332-336, 1990
A>Title: Specific expression of a tyrosine kinase gene, blk, in B lymphoid cells.
A:Reference number: A40092; MUID:90117147; PMID:2404338
A:Accession: A40092
A:Molecule type: mRNA
A:Residues: 1-499 <DYM>
A:Cross-references: GB:M30903; NID:g202076; P1DN:AAA40453.1; PID:g202077
C:Genetics:
A:Gene: MGI:BLK
A:Map position: 14:28.0
C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology; ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F:59-107/Domain: SH3 homology <SH3>
F:118-214/Domain: SH2 homology <SH2>
F:233-491/Domain: protein kinase homology <KIN>
F:241-249/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:263/Active site: Lys #status predicted

Query Match

25.7%; Score 345.5; DB 1; Length 499;
Best Local Similarity 40.5%; Pred. No. 9,2e-21;

Matches 75; Conservative 29; Mismatches 64; Indels 17; Gaps 3;

Qy 11 PPSLSSVGGCPVTMEERSKATNAVALGSPAGAPALSLRLGEPPLTVSBDQDMWTV 70
Db 44 PSPN-----QDPDEBERFVALFDYAAVDDLDQLVGEKQLQVLSSTDWMLA 91
Qy 71 LSEVSGREYNIPSVHAKVS---HGLYEGLSREKAEELLILGNCGAFLIRRSQRR 126
Db 92 RSLVTGREGVPSNFAVAPETLEVEKFFRTIRKDAEROLLAMAKAGSFLIRSSSNK 151
Qy 127 GSYSLVRLSRPASMDRIRHRIHCDNGLYISPLTFPSLQALVDHYSELADICLL 186
Db 132 GAFSLVYK-DITTOGSEVYKIRSLDNGCYISPRITFPTLQALVHYSKKGDLCKL 210
Qy 187 KEPCV 191
Db 211 TLPCV 215

RESULT 10

OKHUK

protein-tyrosine kinase (EC 2.7.1.112) lck - human
N:Alternate names: kinase-related transforming protein (lck)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 28-Jan-2000
C:Accession: J00152; S07822; S07200; S01879; S07143; A32797; I57636
R:Rover, E.; Van Huyen, T.; de Souza, S.L.; Lang, W.C.; Fischer, S.; Benarous, R.
Gene 84, 105-113, 1989
A>Title: Structure of the human lck gene: differences in genomic organisation within src
A:Reference number: J00152; MUID:90108697; PMID:2558056
A:Accession: J00152
A:Molecule type: DNA
A:Residues: 1-509 <ROU>
A:Cross-references: EMBL:X14053
R:Perlmutter, R.M.; Marsh, J.D.; Lewis, D.B.; Peet, R.; Ziegler, S.F.; Wilson, C.B.
J. Cell. Biochem. 38, 117-126, 1988
A>Title: Structure and expression of lck transcripts in human lymphoid cells.
A:Reference number: S07822; MUID:89123626; PMID:3265417
A:Accession: S07822

A:Molecule type: mRNA
A:Residues: 1-86; 'P', 88-509 <PER>
A:Cross-references: EMBL:X13529; NID:g34294; P1DN:CAA1884.1; PID:g34295
R:Koga, Y.; Caccia, N.; Toyonaga, B.; Spolek, R.; Yamagi, Y.; Yoshikai, Y.; Mak, T.W.
Eur. J. Immunol. 16, 1643-1646, 1986
A>Title: A human T cell-specific cDNA clone (YT16) encodes a protein with extensive hom

A:Reference number: S07200; MUID:87133831; PMID:3493153
A:Accession: S07200

A:Molecule type: mRNA
A:Residues: 1-205; 'ASAIRP', 212-257; 'RCGW', 262; 'TTT', 266; 'T', 268-281; 'AGRLP', 287-503; 'ST

A:Cross-references: EMBL:X05027; NID:g36807; P1DN:CAA28591.1; PID:g36808
R:Veilleux, A.; Foss, F.M.; Sauvillie, E.A.; Bolen, J.B.; Rosen, N.
Oncogene Res. 1, 357-374, 1987

A>Title: Expression of the lck tyrosine kinase gene in human colon carcinoma and other t

A:Reference number: S01879; MUID:88217332; PMID:2855736
A:Accession: S01879

A:Molecule type: mRNA
A:Residues: 368-471; 'H', 473-509 <VEI>
A:Cross-references: EMBL:X06369; NID:g34288; P1DN:CAA29667.1; PID:g34289

R:Trevillian, J.M.; Lin, Y.; Chen, S.J.; Phillips, C.A.; Canna, C.; Ilna, T.J.
Biochim. Biophys. Acta 888, 286-295, 1986

A>Title: Human T lymphocytes express a protein-tyrosine kinase homologous to p56 (LSTRA)

A:Reference number: S07143; MUID:87000726; PMID:3489486
A:Accession: S07143

A:Molecule type: mRNA
A:Residues: 'A', 376-509 <TRE>

A:Cross-references: EMBL:X04476; NID:g35779; P1DN:CAA28165.1; PID:g35780
R:Takadera, T.; Leung, S.; Gernone, A.; Koga, Y.; Takihara, Y.; Miyamoto, N.G.; Mak, T.W.

Mo. Cell. Biol. 9, 2173-2180, 1989
A>Title: Structure of the two promoters of the human lck gene: differential accumulation

A:Reference number: A32797; MUID:89313764; PMID:2787474
A:Accession: A32797

A:Molecule type: DNA
A:Residues: 1-35 <TAK>

A:Cross-references: GB:M2692; NID:g341523; P1DN:AAA59503.1; PID:g349702
R:Garvin, A.M.; Pawar, S.; Marsh, J.D.; Perlmutter, R.M.

Mo. Cell. Biol. 8, 3058-3064, 1988
A>Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma cell

A:Reference number: I57636; MUID:89096921; PMID:2850479
A:Accession: I57636

A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-35; 'VR', <RES>
A:Cross-references: GB:M21510; NID:g187031; P1DN:AAA59501.1; PID:g553522

C:Comment: Protein tyrosine kinases play important roles in the control of cell growth a

C:Genetics:
A:Gene: GDB:LCK
A:Cross-references: GDB:119360; OMIM:153390

A:Map position: 1p35-1p34.3
A:Insertions: 35/3; 63/1; 93/2; 126/2; 161/1; 211/1; 262/1; 322/1; 347/3; 399/1; 443/1

C:Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology; ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho

F:2-509/Product: protein-tyrosine kinase lck #status predicted <MAT>
F:68-116/Domain: SH3 homology <SH3>

F:127-224/Domain: SH2 homology <SH2>
F:243-501/Domain: protein kinase homology <KIN>

F:251-259/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F:3,5/Binding site: palmitate (Cys) (covalent) #status predicted
F:273/Active site: Lys #status predicted

F:394,505/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 25.6%; Score 344; DB 1; Length 509;
Best Local Similarity 41.1%; Pred. No. 1.3e-20;

Matches 74; Conservative 26; Mismatches 70; Indels 10; Gaps 2;

Qy 25 VTMEERSKAT-----AVAGSPAGAPALSLRLGEPPLTVSBDQDMWTVLSEVSGRE 78
Db 49 VTVEGSPAPSLQDNVIALSHYSPSHDGLGKEGQRLRLDSGGMWMAQSLLTTCGE 108
Qy 79 YNIPSVHAKVS-----HGLYEGLSREKAEELLILGNCGAFLIRRSQRRGYSLSVR 134


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Query Match      24.1%; Score 324; DB 1; Length 528;
Best local Similarity 31.8%; Pred. No. 5,9e-19;
Matches 92; Conservative 43; Mismatches 104; Indels 50; Gaps 9;

QY   1 GSLSPRKRSLLSPSLSSVVGCGPVTMEAKRSKATAVALGSPFAGPAELSLRLGEPLTT 60
Db   62 GGASSSFSAVPSFYPSTLTGGGT-----PALLDYEARITDGLSKKGGERFOI 110
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY   61 VSE-DGDMMTLTLESEVSGREYNIPSVHAKV----SHGLTEGSEPKAEELLTPGRPG 115
    ::::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Db   111 INNTGGDMWEARSATGKTGYIPSNVAPADISIAEEMYGKKGRDAERLLLPNGQRG 170
    ::::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY   116 AFLIESQTRGCSLSLVLRSPASWDRI---AHRICLNGMLYSPLTFPSLOA 170
    ::::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

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QY      37 VALGSGPAGGAPALSLRIGEDPLIVSE -GDDMMVLSEVSGREXNIPSYHAAKY-----SH 91
D      91 VALVDYARTTEBLSFRKGESEFOIINNTGDMWEARSATGCKGYIPSYNVAAPDSIQAE 150
QY      92 GWLVEGSEFRKABELLLLPNGPGAPFLIRESGTRGSYSLSVRLSPASMPDRIR-----H 146
D      151 EWYFGKGRKDAERLLNLPNGQGRTFLVRESSTTKGAYLSIR-----DMVEYGVGDVNGH 205
QY      147 YRIHCLLNGMLYLSRLFFESQLQVLDHSELAIDICLLKKEC-----VLQAGE 197
D      206 YKIKRLDNGSYITTRAPESLQALYKHSSEHABDCLRLTLVCPPIYKPRQTOGIADKAME 265
QY      199 LPKGDITFLPTVYOR-----TPLNMKELDSSLJFSEAAATGESLSJEGLRBS 243
D      266 IPRSLSLADVKQGGCCGSEFWIGTNGTGTAKAIKTLKPGTMMEEAFLEQAOIMKRLHDK 325
QY      244 L-SFYISLNDNAV 255
D      326 LVPLVAVVSEEP 338

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